



SEQUENCE LISTING

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<120> Genes of purine biosynthesis from Ashbya Gossypii and the use thereof in microbial riboflavin synthesis

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<140> US 10/076,157

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Ser Ile Arg Asp Glu Asp Val Tyr Ile Ile Gln Thr Gly Thr Gly Glu 55

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Val	Ser	Thr 275		Thr	Val	Pro	Val 280		Leu	. Asn	Leu	Asp 285	Ile	Tyr	His
Gln	Ile 290		Ile	Ser	Ala	. Ile 295	Leu	Ala	Glu	Ala	. Il∈ 300	Arg	Arg	Leu	His
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Gln His Arg Phe His Lys Pro Arg Ser	Glu Asp Tyr Ala Tyr Glu Phe
1300 1305	1310 1315

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Arg Phe Arg Arg Asp Ala Asn Lys Ala Asp Asn Lys Ala Ala Ser Val	

Ala Leu Asp Ser Leu Ile Asn Phe Glu Ala Val Lys Tyr Phe Asn Asn

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Ile	Asn	Gln	Leu	Val 165	Phe	Gln	Leu	Ser	Val 170	Pro	Leu	Asn	Phe	Leu 175	Gly
Ser	Val	Tyr	Arg 180	Asp	Leu	Lys	Gln	Ser 185	Leu	Ile	Asp	Met	Glu 190	Ser	Leu
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Va.	1 Let 370		ı Lys	a Asp	Ala	375		u Met	t Phe	e Ph€	28£	Gli	ı Ala	a Thi	r Ser
Ala 38!		ı As _l	p Thi	r His	390	Glu	ı Gl	n Ala	a Lei	u Lei 395	ı His	s Th	r Ile	e Glı	n Glr 400
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Arg Thr Ile Ala Asp Ala Asp Lys Ile Ile Val Leu Glu Gln Gly Ser 420 425 430

Val Arg Glu Glu Gly Thr His Ser Ser Leu Leu Ala Ser Gln Gly Ser 435 440 445

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Cys Lys Gly Asn Gly Met Ala Arg Asp Val Phe Thr Gln Ala Arg Met 50 55

Ser Gly Leu Val Gly Ser Met Gly Ile Ala His Leu Arg Tyr Pro Thr 65 70 75 80

Ala Gly Ser Ser Ala Asn Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser 85 90 95

Pro Tyr Gly Ile Cys Met Ser His Asn Gly Asn Leu Val Asn Thr Met 100 105 110

Ser Leu Arg Arg Tyr Leu Asp Glu Asp Val His Arg His Ile Asn Thr 115 120 125

Asp Ser Asp Ser Glu Leu Leu Leu Asn Ile Phe Ala Ala Glu Leu Glu 130 135 140

Lys Tyr Asn Lys Tyr Arg Val Asn Asn Asp Asp Ile Phe Cys Ala Leu 145 150 155 160

Glu Gly Val Tyr Lys Arg Cys Arg Gly Gly Tyr Ala Cys Val Gly Met 165 170 175

Leu Ala Gly Tyr Gly Leu Phe Gly Phe Arg Asp Pro Asn Gly Ile Arg 180 185 190

Pro Leu Leu Phe Gly Glu Arg Val Asn Asp Asp Gly Thr Met Asp Tyr 195 200 205

Met Leu Ala Ser Glu Ser Val Val Leu Lys Ala His Arg Phe Gln Asn 210 Ile Arg Asp Ile Leu Pro Gly Gln Ala Val Ile Ile Pro Lys Thr Cys Gly Ser Ser Pro Pro Glu Phe Arg Gln Val Val Pro Ile Glu Ala Tyr Lys Pro Asp Leu Phe Glu Tyr Val Tyr Phe Ala Arg Ala Asp Ser Val Leu Asp Gly Ile Ser Val Tyr His Thr Arg Leu Leu Met Gly Ile Lys Leu Ala Glu Asn Ile Lys Lys Gln Ile Asp Leu Asp Glu Ile Asp Val Val Val Ser Val Pro Asp Thr Ala Arg Thr Cys Ala Leu Glu Cys Ala Asn His Leu Asn Lys Pro Tyr Arg Glu Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile Met Pro Asn Gln Lys Glu Arg Val Ser Ser Val Arg Arg Lys Leu Asn Pro Met Asn Ser Glu Phe Lys Asp Lys Arg Val Leu Ile Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Lys Glu Ile Val Asn Met Ala Lys Glu Ser Gly Ala Ala Lys Val Tyr Phe Ala Ser Ala Ala Pro Ala Ile Arg Phe Asn His Ile Tyr Gly Ile Asp Leu Ala Asp Thr Lys Gln Leu Val Ala Tyr Asn Arg Thr Val Glu Glu Ile Thr Ala Glu Leu Gly Cys Asp Arg Val Ile Tyr Gln Ser Leu Asp Asp Leu Ile Asp Cys Cys Lys Thr Asp Ile Ile Ser Glu Phe Glu Val Gly Val Phe Thr Gly Asn Tyr Val Thr Gly Val Glu Asp Val Tyr Leu Gln Glu Leu Glu Arg Cys Arg Ala Leu Asn Asn Ser Asn Lys Gly Glu Ala Lys Ala Glu Val Asp Ile Gly Leu Tyr Asn Ser Ala Asp Tyr 505

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Gly Asp Ser Asn Lys Ala Ile 305 310	Ser Val Thr	Gln His Arg Phe 315	His Lys 320
Pro Arg Ser Glu Asp Tyr Ala 325	Tyr Glu Phe 0	Glu Leu Pro Ser	Lys His 335
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ccg Pro	g aco	c Gly	g aaq y Ly:	g ctg s Lei 160	ı Glr	g 999 n Gly	g ato / Ile	c ato	c acq e Thi 16!	r Sei	c cgi	t gad g Asj	c ato o Ilo	c cag e Gli 17	g ttt n Phe O	1537
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Asn Gln Ile Leu Lys Asn Thr Lys Lys Gly Lys Leu Pro Ile Val Asp

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ggggatga												420
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cct ttg cgc gag ctt ttc aag gac gag gtg aga cac ctg gga gaa cta Pro Leu Arg Glu Leu Phe Lys Asp Glu Val Arg His Leu Gly Glu Leu 375 380 385 390	
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